

ESD Ecology Department Publications, 2007–2011

2011

ESD Ecology Department Peer-Reviewed Journal Articles, Books, and Book Chapters for 2011

1. Beller, H.R., T.C. Legler, and S.R. Kane (2012), Genetic manipulation of the obligate chemolithoautotrophic bacterium *Thiobacillus denitrificans*. In: Microbial Systems Biology: Methods and Protocols, A. Navid, ed., Humana Press, Methods in Molecular Biology series (in press). LBNL-5097E.
2. Borglin, S. D. Joyner, K. DeAngelis, J. Khudyakov, P. D'haeseleer, M.P. Joachimiak, and T.C. Hazen (2012), Application of phenotypic microarrays to environmental microbiology. *Current Opinion in Biotechnology*, 23, 41–48; DOI: 10.1016/j.copbio.2011.12.006.
3. Chakraborty, R., C.H. Wu, and T.C. Hazen (2012), Systems biology approach to bioremediation. *Current Opinion in Biotechnology*, 23, 1–8; DOI: 10.1016/j.copbio.2012.01.015.
4. DeAngelis, K., J.L. Fortney, S. Borglin, W.L. Silver, B.A. Simmons, and T.C. Hazen (2012), Anaerobic decomposition of switchgrass by tropical soil-derived feedstock adopted consortia. *mBio*, 3 (1), e00249-11; DOI: 10.1128/mBio.00249-11.
5. Dong, W., T.K. Tokunaga, J.A. Davis, and J. Wan (2012), Uranium(VI) adsorption and surface complexation modeling onto background sediments from the F-Area Savannah River site. *Environmental Science & Technology*, 46, 1565–1571; DOI: 10.1021/es2036256.
6. Goh, E.-B., E.E.K. Baidoo, J.D. Kiesling, and H.R. Beller (2012), Engineering of bacterial methyl ketone synthesis for biofuels. *Applied and Environmental Microbiology*, 78 (1), 70–80; DOI: 10.1128/AEM.06785-11. LBNL-5120E.
7. Lu, Z., Y. Deng, J.D. Van Nostrand, Z. He, J. Voordeckers, A. Zhou, Y.-J. Lee, O.U. Mason, E. Dubinsky, K. Chavarria, L. Tom, J. Fortney, R. Lamendella, J.K. Jansson, P. D'haeseleer, T.C. Hazen, and J. Zhou (2012), Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. *ISME Journal*, 6 (2), 451–60; DOI: 10.1038/ismej.2011.91. LBNL-5055E.
8. Mason, O.U., T.C. Hazen, S. Borglin, P. Chain, E. A. Dubinsky, J. Fortney, J. Han, J. Hultman, R. Lamendella, R. Mackelprang, L. M. Tom, S. G. Tringe, T. Woyke, J. Zhou, E. M. Rubin, and J.K. Jansson (2012), Multi-omics approach reveals a chemotactic response by dominant, aliphatic hydrocarbon degrading bacteria to the Deepwater Horizon deep-sea plume. *Nature* (in press).
9. Mayali, X., P.K. Weber, E.L. Brodie, S. Mabery, P.D. Hoeprich, and J. Pett-Ridge (2012), High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. *ISME Journal*, DOI: 10.1038/ismej.2011.175.

2011

ESD Peer-Reviewed Journal Articles and Book Chapters for 2011

1. Atlas, R., and T.C. Hazen (2011), Oil biodegradation and bioremediation: A tale of the two worst spills in U.S. history. *Environmental Science & Technology*; DOI: 10.1021/es2013227. LBNL-5069E.
2. Barkouki, T.H., B.C. Martinez, B.M. Mortensen, T.S. Weathers, J.D. De Jong, T.R. Ginn, N.F. Spycher, R.W. Smith, and Y. Fujita (2011), Forward and inverse biogeochemical modeling of microbially induced calcite precipitation in half-meter column experiments. *Transport in Porous Media*, 90 (1), 23–29; DOI: 10.1007/s11242-011-9804-z, 1–17.
3. Beller, H.R., T.C. Legler, and S.R. Kane. (2011) Genetic manipulation of the obligate chemolithoautotrophic bacterium *Thiobacillus denitrificans*. In: *Microbial Systems Biology: Methods and Protocols*, A. Navid, ed., Humana Press, Methods in Molecular Biology series (in press). LBNL-5097E.
4. Beller, H.R., E.-B. Goh, and J.D. Keasling (2011), Definitive alkene identification need for in vitro studies with Ole (olefin biosynthesis) proteins. *Journal of Biological Chemistry* (letter), 286 (26), le11. LBNL-5054E.
5. Brodie, E.L., D.C. Joyner, B. Faybushenko, M.E. Conrad, C. Rios-Velazquez, B. Mork, R. Kelley, A. Willet, S. Koenigsberg, D. Herman, M.K. Firestone, and T.C. Hazen (2011), Microbial community response to addition of polylactate compounds to stimulate hexavalent chromium reduction in groundwater. *Chemosphere*, 85 (4), 660–665; DOI: 10.1016/j.gca.2011.09.033. LBNL-4905E.
6. Campbell, K.M., J.A. Davis, J. Bargar, D. Giammar, R. Bernier-Latmani, R. Kukkadapu, K.H. Williams, H. Veramani, K.U. Ulrich, J. Stubbs, S. Yabusaki, L. Figueroa, E. Lesher, M.J. Wilkins, A. Peacock, and P.E. Long (2011), Composition, stability, and measurement of reduced uranium phases for groundwater bioremediation at Old Rifle, CO. *Applied Geochemistry*, 26, Supplement: S, S167–169; DOI: 10.1016/j.apgeochem.2011.03.094.
7. Cantarel, B.L., A.R. Erickson, N.C. VerBerkmoes, B.K. Erickson, P.A. Carey, C. Pan, M. Shah, E.F. Mongodin, J.K. Jansson, C.M. Fraser-Liggett, and R.L. Hettich (2011), Strategies for metagenomic-guided whole-community proteomics of complex microbial environments. *PLoS ONE*, 6 (11), e27173. DOI:10.1371/journal.pone.0027173.
8. Chakraborty, R., T.C. Hazen, D.C. Joyner, K. Kusel, M.E. Singer, J. Sitte, and T. Torok (2011), Use of immunomagnetic separation for the detection of *Desulfovibrio vulgaris* from environmental samples. *Journal of Microbiological Methods*, 86 (2), 204–209; DOI:10.1016/j.mimet.2011.05.005. LBNL-4925E.
9. Chhabra, S.R., M.P. Joachimiak, C.J. Petzold, G.M. Zane, M.N. Price, S. Gaucher, S.A. Reveco, V. Fok, A.R. Johanson, T.S. Batt, M. Singer, J.M. Chandonia, D. Joyner, T.C. Hazen, A.P. Arkin, J.D. Wall, A.K. Singh, and J.D. Keasling (2011), Towards a rigorous network of protein-protein interactions of the model sulfate reducer *Desulfovibrio vulgaris Hildenborough*. *PLoS One*, 6(6), e21470; DOI:10.1371/journal.pone.0021470. LBNL-5181E.
10. Chhabra, S. R., G. Butland, D. Elias, J.-M. Chandonia, V. Fok, T. Juba, A. Gorur, S. Allen, C.-M. Leung, K. Keller, S. Reveco, G. Zane, E. Semkiw, R. Prathapam, B. Gold, M.

- Singer, M. Ouellet, E. Sazakal, D. Jorgens, M. Price, E. Witkowska, H. Beller, T.C. Hazen, M. Biggin, M. Auer, J. Wall, and J. Keasling (2011), Generalized schemes for high throughput manipulation of the *Desulfovibrio vulgaris* Hildenborough genome. Applied & Environmental Microbiology, 77 (22); DOI: 10.1128/AEM.05495-11. LBNL-5207E.
11. Cooper, M., M.T. La Duc, A. Probst, P. Vaishampayan, C. Stam, J.N. Benardini, Y.M. Piceno, G.L. Andersen, and K. Venkateswaran (2011), Assessing the cleanliness of surfaces: Innovative molecular approaches vs. standard spore assays. Applied and Environmental Microbiology, 77 (15), 5438–5444; DOI:10.1128/AEM.00192-11. LBNL-4946E.
12. DeAngelis, K.M., M. Allgaier, Y. Chavarria, J.L. Fortney, P. Hugenholtz, B. Simmons, K. Sublette, W.L. Silver, and T.C. Hazen (2011), Characterization of trapped lignin-degrading microbes in tropical forest soil. PLoS One, 6 (4), e19306; DOI:10.1371/journal.pone.0019306. LBNL-4834E.
13. DeAngelis, K.M., C.H. Wu, H.R. Beller, E.L. Brodie, R. Chakraborty, T.Z. DeSantis, J.L. Fortney, T.C. Hazen, S.R. Osman, M.E. Singer, L.M. Tom, and G.L. Andersen (2011), PCR amplification-independent methods for detection of microbial communities by the high-density microarray PhyloChip. Applied and Environmental Microbiology, 77 (18), 6313–6322; DOI: 10.1128/AEM.05262-11. LBNL-5336E.
14. DeSantis, T.Z., K. Keller, U. Karaoz, A.V Alekseyenko, N.N.S. Singh, E.L Brodie, Z. Pei, G.L Andersen, and N. Larsen (2011), Simrank: Rapid and sensitive general-purpose k-mer search tool. BMC Ecology, 11 (11); DOI: 10.1186/1472-6785-11-11. LBNL-4596E.
15. Dohnalkova, AC., M.J. Marshall, B.W. Arey, K.H. Williams, E.C. Buck, and J.K. Fredrickson (2011), Imaging hydrated microbial extracellular polymers: Comparative analysis by electron microscopy. Applied and Environmental Microbiology, 77 (4), 1254–1262; DOI:10.1128/AEM.02001-10. LBNL-4861E.
16. Flores-Orozco, A., K.H. Williams, P.E. Long, S.S. Hubbard and A. Kemna (2011), Using spectral induced polarization (SIP) to infer biogeochemical processes associated with bioremediation of a uranium-contaminated aquifer. JGR-Biogeosciences, 116, G03001; DOI:10.1029/2010JG001591. LBNL-4766E.
17. Gladden, J.M., M. Allgaier, C. S. Miller, T.C. Hazen, J.S. VanderGheynst, P. Hugenholtz, B.A. Simmons, and S.W. Singer (2011). Glycoside hydrolase activities of thermophilic bacterial consortia adapted to switchgrass. Applied and Environmental Microbiology, 77 (16), 5804–5812. LBNL-4911E.
18. Goh, E.-B., E.E.K. Baidoo, J.D. Kiesling, and H.R. Beller (2012), Engineering of bacterial methyl ketone synthesis for biofuels. Applied and Environmental Microbiology, 78 (1), 70–80; DOI: 10.1128/AEM.06785-11. LBNL-5120E.
19. Goldfarb, K.C., U. Karaoz, C.A. Hanson, C.A. Santee, M.A. Bradford, K.K. Treseder, M.D. Wallenstein, and E.L. Brodie (2011), Differential growth responses of soil bacterial taxa to carbon substrates of varying chemical recalcitrance. Frontiers in Terrestrial Micobiology, 2 (94); DOI: 10.3389/fmicb.2011.00094. LBNL-4963E.
20. Graham, D.E., M.D. Wallenstein, T. A. Vishnivetskaya, M.P. Waldrop, T.J. Phelps, S.M. Pfiffner, T.C. Onstott, L.G. Whyte, E.M. Rivkina, D.A. Gilichinsky, D.A. Elias, R Mackelprang, N.C. VerBerkmoes, R.L. Hettich, D. Wagner, S.D. Wullschleger, and

- J.K. Jansson (2011), Microbes in thawing permafrost: The unknown variable in the climate change equation. *The ISME Journal*, DOI: 10.1038/ismej.2011.163.
- 21. Jansson, J.K. (2011), Towards “*tera terra*”: Terabase sequencing of terrestrial metagenomics. *Microbe*, July 2011. LBNL-5191E.
 - 22. Jansson, J.K. J.D. Neufeld, M.A. Moran, and J.A. Gilbert (2011), Omics for understanding microbial community dynamics. *Environmental Microbiology*, DOI: 10.1111/j.1462-2920.2011.02518x.
 - 23. Jansson, J.K. (2011), Deep metagenome sequencing illuminates rapid permafrost response to thaw. *Nature Letter* (in press), 2010-12-16310B.
 - 24. Kerkhof, L., K.H. Williams, P.E. Long, and L. McGuinness (2011), Phase preference by acetate-utilizing bacteria during DNA replication at the Rifle, CO, Integrated Field Research Challenge Site. *Environmental Science & Technology*, 45 (4), 1250–1256; DOI: 0.1021/es102893r. LBNL-4853E.
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 - 26. Liang, Y., J.D. Van Nostrand, A.D. Peacock, Y. Deng, P.E. Long, L. Wu, Z. He, T.C. Hazen, G. Li, and J. Zhou (2011), Microarray-based functional analysis of microbial communities for in-situ uranium reduction under sulfate-reducing vs. Fe-reducing conditions. *ISME Journal* (in press).
 - 27. Liu, P., R.J. Meagher, Y.K. Light, S. Yilmaz, R. Chakraborty, A.P. Arkin, T.C. Hazen, and A.K. Singh (2011), Microfluidic fluorescence in situ hybridization and flow cytometry (μ FISH). *Lab on a Chip*, 11 (16), 2673–2679.
 - 28. Lu, Z., Y. Deng, J.D. Van Nostrand, Z. He, J. Voordeckers, A. Zhou, Y.-J. Lee, O.U. Mason, E. Dubinsky, K. Chavarria, L. Tom, J. Fortney, R. Lamendella, J.K. Jansson, P. D’haeseleer, T.C. Hazen, and J. Zhou (2011), Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. *ISME Journal*, DOI: 10.1038/ismej.2011.91. LBNL-5055E.
 - 29. Mackelprang, R., M.P. Waldrop, K.M. DeAngelis, M.M. David, K.L. Chavarria, S.J. Blazewicz, E.M. Rubin, and J.K. Jansson (2011), Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. *Nature*, 480, 368–371; DOI: 10.1038/nature10576. LBNL-5155E.
 - 30. Mason, O.U., T.C. Hazen, S. Borglin, P. Chain, E. A. Dubinsky, J. Fortney, J. Han, J. Hultman, R. Lamendella, R. Mackelprang, L. M. Tom, S. G. Tringe, T. Woyke, J. Zhou, E. M. Rubin, and J.K. Jansson (2011), Multi-omics approach reveals a chemotactic response by dominant, aliphatic hydrocarbon degrading bacteria to the Deepwater Horizon deep-sea plume. *Nature* (in press).
 - 31. Mason, O.U., and T.C. Hazen (2011), New insights into microbial responses to oil spills from the Deepwater Horizon incident. *SIM News*, 16, 60–65. LBNL-5048E.
 - 32. Mayali, X., P.K. Weber, E.L. Brodie, S. Mabery, P.D. Hoeprich, and J. Pett-Ridge (2011), High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. *ISME Journal*, DOI: 10.1038/ismej.2011.175.
 - 33. Men, Y., H. Feil, N.C. VerBerkmoes, M.B. Shah, D.R. Johnson, P.K.H Lee, K.A. West, S.H. Zinder, G.L. Andersen, and L. Alvarez-Cohen (2011), Sustainable syntrophic

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- 34. Miletto, M., K.H. Williams, A.L. N'Guessan, and D.R. Lovley (2011), Molecular analysis of the metabolic rates of discrete subsurface populations of sulfate reducers. Applied and Environmental Microbiology, 77 (18), 6502–6509; DOI: 10.1128/AEM.00576-11. LBNL-4933E.
 - 35. Mohanty, S.R., B. Kollah, E.L. Brodie, T.C. Hazen, and E.E. Roden (2011), 16S rRNA gene microarray analysis of microbial communities in ethanol-stimulated subsurface sediment. Microbes and Environments, 26 (3), 261–265; DOI:10.1264/jsme.ME11111. LBNL-5051E.
 - 36. Nelson, T.A., S. Holmes, A.V. Alekseyenko, M. Shenoy, T. DeSantis, C.H. Wu, G.L. Andersen, J. Winston, J. Sonnenburg, P.J. Pasricha, and A. Spormann (2011), PhyloChip microarray analysis reveals altered gastrointestinal microbial communities in a rat model of colonic hypersensitivity. Neurogastroenterology & Motility, 23 (2), 169–177; DOI: 10.1111/j.1365-2982.2010.01637.x. LBNL-4351E.
 - 37. Paszczynski, A.J., R. Paidisetti, A.K. Johnson, R.L. Crawford, F.S. Colwell, T. Green, M. Delwiche, H. Lee, D. Newby, E.L. Brodie, and M. Conrad (2011), Proteomic and targeted qPCR analyses of subsurface microbial communities for presence of methane monooxygenase. Biodegradation, 22 (6): 1045–1059, DOI: 10.1007/s10532-011-9462-4.
 - 38. Reddy, A.P., M. Allgaier, S.W. Singer, T.C. Hazen, B.A. Simmons, P. Hugenholtz, and J.S. VanderGheynst (2011), Bioenergy feedstock-specific enrichment of microbial populations during high-solids thermophilic deconstruction. Biotechnology & Bioengineering, 108 (9), 2088–2098; DOI:10.1002/bit.23176. LBNL-4922E.
 - 39. Reindl, W., K. Deng, J. M. Gladden, G. Cheng, A. Wong, S. W. Singer, S. Singh, J.-C. Lee, J.-S. Yao, T. C. Hazen, A. K Singh, B. A. Simmons, P. D. Adams, and T. R. Northen (2011), Colloid-based multiplexed method for screening plant biomass-degrading glycoside hydrolase activities in microbial communities. Energy & Environmental Science, 4, 2884–2893. LBNL-5216E.
 - 40. Scheibe, T., S.S. Hubbard, T.C. Onstott, and M.F. DeFlaun (2011), Lessons learned from bacterial transport research at the South Oyster Field Research Site. Ground Water, 49(5), 745–763; DOI: 10.1111/j.1745-6584.2011.00831.x. LBNL-4756E.
 - 41. Singer, S. W., A. P. Reddy, J. M. Gladden, H. Guo, T.C. Hazen, B. A. Simmons, and J. S. VanderGheynst (2011), Enrichment, isolation and characterization of fungi tolerant to 1-ethyl-3-methylimidazolium acetate. Journal of Applied Microbiology, 110, 1023–1031. LBNL-4924E.
 - 42. Spycher, N., M. Issarangkun, B. Stewart, S.S. Sengor, E. Belding, T. Ginn, B. Peyton, and R.K. Sani (2011), Biogenic uraninite precipitation and its reoxidation by iron(III) (hydr)oxides: A reaction modeling approach. Geochimica et Cosmochimica Acta, 75 (16), 4426–4440; DOI: 10.1016/j.gca.2011.05.008. LBNL-4605E.
 - 43. Stewart, B.D., R.T. Amos, P.S. Nico, and S. Fendorf (2011), Influence of uranyl speciation and iron oxides on uranium biogeochemical redox reactions. Geomicrobiology Journal, 28, 444–456; DOI: 10.1080/01490451.2010.507646. LBNL-3549E.

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46. Swarbreck, S.M., E.A. Suderth, S.B. St.Clair, R. Salve, C. Castanha, M.S. Torn, D.D. Ackerly, and G.L. Andersen (2011), Linking leaf transcripts levels to whole plant analyses provides mechanistic insights to the impact of warming and altered water availability in an annual grass. *Global Change Biology*, 17 (4), 1577–1594; DOI: 10.1111/j.1365-2486.2010.02359.x.
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48. Weber, K.A., J.C. Thrash, J.I. Van Trump, L.A. Achenbach, and J.D. Coates (2011), Environmental and taxonomic bacterial diversity of anaerobic uranium(IV) bio-oxidation. *Applied and Environmental Microbiology*, 77 (13), 4693-4696; DOI: 10.1128/AEM.02539-10.
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50. Williams, K.H., P.E. Long, J.A. Davis, C.I. Steefel, M.J. Wilkins, A.L. N'Guessan, L. Yang, D. Newcomer, F.A. Spane, L.J. Kerkhof, L. McGuinness, R. Dayvault, and D.R. Lovely (2011), Acetate availability and its influence on sustainable bioremediation of uranium-contaminated groundwater. *Geomicrobiology Journal*, 28 (5–6), 519–539; DOI: 10.1080/01490451.2010.520074. LBNL-4622E.
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2010

Ecology Department Peer-Reviewed Journal Articles, Books, and Book Chapters for 2010

1. Allgaier, M., A. Reddy, J. I. Park, N. Ivanova, P. D'haeseleer, S. Lowry, R. Sapra, T.C. Hazen, B.A. Simmons, J. S. VanderGheynst, and P. Hugenholtz (2010), Targeted discovery of glycoside hydrolases from a switchgrass-adapted compost community. LBNL-3058E. *PLoS One*, 5 (1), e8812.
2. Andersen, G.L., Z. He, T.Z. DeSantis, E.L. Brodie, and J. Zhou (2010), The use of microarrays in microbial ecology. LBNL-3263E. In: *Environmental Molecular Microbiology*, Chapter 5, W.-T. Liu and J.K. Jansson (eds.), Caister Academic Press.
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